



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/876,187

DATE: 03/25/2002 8.5

TIME: 14:52:22

Input Set : A:\LJ4714.txt

Output Set: N:\CRF3\03252002\I876187.raw

```

4 <110> APPLICANT: Lipton, Stuart A.
5   Okamoto, Shu-ichi
7 <120> TITLE OF INVENTION: Methods of Differentiating and
8   Protecting Cells By Modulating the P38/MEF2 Pathway
11 <130> FILE REFERENCE: P-LJ 4714
13 <140> CURRENT APPLICATION NUMBER: US 09/876,187
C--> 14 <141> CURRENT FILING DATE: 2002-03-12
16 <150> PRIOR APPLICATION NUMBER: US 60/209,539
17 <151> PRIOR FILING DATE: 2000-06-05
19 <160> NUMBER OF SEQ ID NOS: 23
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 2975
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (415)...(1935)
32 <400> SEQUENCE: 1
33 gaattttctg caaggatcat atctaagtgc actttttgct gatacttcat ttctagacat 60
34 tgagtctcac totaccccc aggctgaagt gcagtgggtg gatctcggtt cactgcaacc 120
35 tccgcctcca ggttcaagtg attctcgtac ctcagcctcc cgagtagctg ggattacagg 180
36 cgctgccac catgcctggc tgatatttat atttttagta gagatggagt ttcaccatgt 240
37 tggccaggct ggtctcgaac tctggacctc agatcttgta gaaaatttca gctgtagccc 300
38 ttggactaga agctgaaata acagaagctg tgtacgatgc attagggtat tgaagaaaaa 360
39 taacttttga attaaatatt tggaatataa ggaaataagg aaagttgact gaaa atg 417
40                                     Met
41                                     1
43 ggg cgg aag aaa ata caa atc aca cgc ata atg gat gaa agg aac cga 465
44 Gly Arg Lys Lys Ile Gln Ile Thr Arg Ile Met Asp Glu Arg Asn Arg
45           5                      10                      15
47 cag gtc act ttt aca aag aga aag ttt gga tta atg aag aaa gcc tat 513
48 Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala Tyr
49           20                      25                      30
51 gaa ctt agt gtg ctc tgt gac tgt gaa ata gca ctc atc att ttc aac 561
52 Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe Asn
53           35                      40                      45
55 agc tct aac aaa ctg ttt caa tat gct agc act gat atg gac aaa gtt 609
56 Ser Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys Val
57 50                      55                      60                      65
59 ctt ctc aag tat aca gaa tat aat gaa cct cat gaa agc aga acc aac 657
60 Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr Asn
61           70                      75                      80

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63	tcg gat att gtt gag gct ctg aac aag aag gaa cac aga ggg tgc gac	705
64	Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys Asp	
65	85 90 95	
67	agc cca gac cct gat act tca tat gtg cta act cca cat aca gaa gaa	753
68	Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu Glu	
69	100 105 110	
71	aaa tat aaa aaa att aat gag gaa ttt gat aat atg atg cgg aat cat	801
72	Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Met Arg Asn His	
73	115 120 125	
75	aaa atc gca cct ggt ctg cca cct cag aac ttt tca atg tct gtc aca	849
76	Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val Thr	
77	130 135 140 145	
79	gtt cca gtg acc agc ccc aat gct ttg tcc tac act aac cca ggg agt	897
80	Val Pro Val Thr Ser Pro Asn Ala Leu Ser Tyr Thr Asn Pro Gly Ser	
81	150 155 160	
83	tca ctg gtg tcc cca tct ttg gca gcc agc tca acg tta aca gat tca	945
84	Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp Ser	
85	165 170 175	
87	agc atg ctc tct cca cct caa acc aca tta cat aga aat gtg tct cct	993
88	Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser Pro	
89	180 185 190	
91	gga gct cct cag aga cca cca agt act ggc aat gca ggt ggg atg ttg	1041
92	Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met Leu	
93	195 200 205	
95	agc act aca gac ctc aca gtg cca aat gga gct gga agc agt cca gtg	1089
96	Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro Val	
97	210 215 220 225	
99	ggg aat gga ttt gta aac tca aga gct tct cca aat ttg att gga gct	1137
100	Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly Ala	
101	230 235 240	
103	act ggt gca aat agc tta ggc aaa gtc atg cct aca aag tct ccc cct	1185
104	Thr Gly Ala Asn Ser Leu Gly Lys Val Met Pro Thr Lys Ser Pro Pro	
105	245 250 255	
107	cca cca ggt ggt ggt aat ctt gga atg aac agt agg aaa cca gat ctt	1233
108	Pro Pro Gly Gly Gly Asn Leu Gly Met Asn Ser Arg Lys Pro Asp Leu	
109	260 265 270	
111	cga gtt gtc atc ccc cct tca agc aag ggc atg atg cct cca cta tcg	1281
112	Arg Val Val Ile Pro Pro Ser Ser Lys Gly Met Met Pro Pro Leu Ser	
113	275 280 285	
115	gag gaa gag gaa ttg gag ttg aac acc caa agg atc agt agt tct caa	1329
116	Glu Glu Glu Glu Leu Leu Asn Thr Gln Arg Ile Ser Ser Ser Gln	
117	290 295 300 305	
119	gcc act caa cct ctt gct acc cca gtc gtg tct gtg aca acc cca agc	1377
120	Ala Thr Gln Pro Leu Ala Thr Pro Val Val Ser Val Thr Thr Pro Ser	
121	310 315 320	
123	ttg cct ccg caa gga ctt gtg tac tca gca atg ccg act gcc tac aac	1425
124	Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr Asn	
125	325 330 335	
127	act gat tat tca ctg acc agc gct gac ctg tca gcc ctt caa ggc ttc	1473

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128 Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly Phe
129          340          345          350
131 aac tcg cca gga atg ctg tcg gga cag gtg tcg gcc tgg cag cag 1521
132 Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln Gln
133          355          360          365
135 cac cac cta gga caa gca gcc ctc agc tct ctt gtt gct gga ggg cag 1569
136 His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly Gln
137 370          375          380          385
139 tta tct cag ggt tcc aat tta tcc att aat acc aac caa aac atc agc 1617
140 Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile Ser
141          390          395          400
143 atc aag tcc gaa ccg att tca cct cct cgg gat cgt atg acc cca tcg 1665
144 Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro Ser
145          405          410          415
147 ggc ttc cag cag cag cag cag cag cag cag cag cag cag ccg ccg cca 1713
148 Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro
149          420          425          430
151 cca ccg cag ccc cag cca caa ccc ccg cag ccc cag ccc cga cag gaa 1761
152 Pro Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Gln Pro Arg Gln Glu
153          435          440          445
155 atg ggg cgc tcc cct gtg gac agt ctg agc agc tct agt agc tcc tat 1809
156 Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser Tyr
157 450          455          460          465
159 gat ggc agt gat cgg gag gat cca cgg ggc gac ttc cat tct cca att 1857
160 Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro Ile
161          470          475          480
163 gtg ctt ggc cga ccc cca aac act gag gac aga gaa agc cct tct gta 1905
164 Val Leu Gly Arg Pro Pro Asn Thr Glu Asp Arg Glu Ser Pro Ser Val
165          485          490          495
167 aag cga atg agg atg gac gcg tgg gtg acc taaggcttcc aagctgatgt 1955
168 Lys Arg Met Arg Met Asp Ala Trp Val Thr
169          500          505
171 ttgtactttt gtgttactgc agtgacctgc cctacatatc taaatcggtg aataaggaca 2015
172 tgagttaaat atatttatat gtacatacat atatatatcc ctttacatat atatgtatgt 2075
173 ggggtgtgagt gtgtgtgtat gtgtgggtgt gtgtttacata cacagaatca ggcacttacc 2135
174 tgcaaaactcc ttgtaggtct gcagatgtgt gtcccatggc agacaaagca ccctgtaggc 2195
175 acagacaagt ctggcacttc cttggactac ttgtttcgta aagataacca gtttttgtag 2255
176 agaaacgtgt acccatatat aattctoccca cactagcttg cagaaaccta gagggccccc 2315
177 tacttgtttt atttaactgt gcagtgactg tagttactta agagaaaatg cttttagtag 2375
178 cagagcagta gaaaagcagg aaccaagaaa gcaataactgt acataaaatg tcatttatat 2435
179 ttccaacctt ggcattgggtg tctgttgcaa aggggtgcat gggaaagggc tgttgatatt 2495
180 aaaaacaaac aaaacaaaaa agccccacac ataactgttt tgcacgtgca aaaatgtatt 2555
181 ggggtcaagaa gtgatcttta gctaataaag aaagagaata gaaaacacgc atgagatatt 2615
182 cagaaaatac tagcctagaa atatagagca ttaacaaagg aaaattaata tattaagtta 2675
183 taattggaat atgtcagaag tttcttttta cattcatatc ttaaaaatta aagaaactga 2735
184 ttttagctca tgtatatatt atatgaaaga aaacaccctt atgaattgat gactatatat 2795
185 aaaattatat tcactacttt tgaacacatt ctgctatgaa ttatttatat aagccaaagc 2855
186 tatatgttgt aacttttttt tagagaatag ctttatcttg gtttaactct ttagttttat 2915
187 tttaagaggg gaaaacaaaa atatcttgca agcagaacct tgaaaaaaa aaaggaattc 2975

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190 <210> SEQ ID NO: 2
191 <211> LENGTH: 507
192 <212> TYPE: PRT
193 <213> ORGANISM: Homo sapiens
195 <400> SEQUENCE: 2
196 Met Gly Arg Lys Lys Ile Gln Ile Thr Arg Ile Met Asp Glu Arg Asn
197 1 5 10 15
198 Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala
199 20 25 30
200 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
201 35 40 45
202 Asn Ser Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
203 50 55 60
204 Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
205 65 70 75 80
206 Asn Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys
207 85 90 95
208 Asp Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu
209 100 105 110
210 Glu Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Met Arg Asn
211 115 120 125
212 His Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val
213 130 135 140
214 Thr Val Pro Val Thr Ser Pro Asn Ala Leu Ser Tyr Thr Asn Pro Gly
215 145 150 155 160
216 Ser Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp
217 165 170 175
218 Ser Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser
219 180 185 190
220 Pro Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met
221 195 200 205
222 Leu Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro
223 210 215 220
224 Val Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly
225 225 230 235 240
226 Ala Thr Gly Ala Asn Ser Leu Gly Lys Val Met Pro Thr Lys Ser Pro
227 245 250 255
228 Pro Pro Pro Gly Gly Gly Asn Leu Gly Met Asn Ser Arg Lys Pro Asp
229 260 265 270
230 Leu Arg Val Val Ile Pro Pro Ser Ser Lys Gly Met Met Pro Pro Leu
231 275 280 285
232 Ser Glu Glu Glu Glu Leu Glu Leu Asn Thr Gln Arg Ile Ser Ser Ser
233 290 295 300
234 Gln Ala Thr Gln Pro Leu Ala Thr Pro Val Val Ser Val Thr Thr Pro
235 305 310 315 320
236 Ser Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr
237 325 330 335
238 Asn Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly
239 340 345 350

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240 Phe Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln
241           355                      360                      365
242 Gln His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly
243       370                      375                      380
244 Gln Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile
245 385                      390                      395                      400
246 Ser Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro
247           405                      410                      415
248 Ser Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro
249           420                      425                      430
250 Pro Pro Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Gln Pro Arg Gln
251       435                      440                      445
252 Glu Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser Ser
253       450                      455                      460
254 Tyr Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro
255 465                      470                      475                      480
256 Ile Val Leu Gly Arg Pro Pro Asn Thr Glu Asp Arg Glu Ser Pro Ser
257           485                      490                      495
258 Val Lys Arg Met Arg Met Asp Ala Trp Val Thr
259       500                      505
262 <210> SEQ ID NO: 3
263 <211> LENGTH: 1671
264 <212> TYPE: DNA
265 <213> ORGANISM: Homo sapiens
267 <220> FEATURE:
268 <221> NAME/KEY: CDS
269 <222> LOCATION: (443)...(1537)
271 <400> SEQUENCE: 3
272 cgggggtcgc tatggaggag ccggagatgc agctcaaggg gaagaaagtc acggacaagt 60
273 tcaactgagag cgtctacgtc ctggccaacg agccatccgt ggcctgttac cggctgcagg 120
274 agcatgtgcg tcgtccctc cccgagctgg ccagacacaa ggcagacatg cagcgttggg 180
275 aggagcagag ccagggagcc atctacactg tggagtacgc ctgcagcgcc gtgaagaacc 240
276 tgggtggacag cagcgtctac ttccgcagcg tggagggtct gctcaaacag gccatcagca 300
277 tccgggacca tatgaatgcc agtgcccagg gccacagccc ggaggaacca ccccgccct 360
278 cctcagcctg atcctggaag agactcgggg ccccccagcc tccgccaacc cagacaaaga 420
279 tcattccact cagcctggga cg atg ggg agg aaa aaa atc cag atc tcc cgc 472
280           Met Gly Arg Lys Lys Ile Gln Ile Ser Arg
281           1                      5                      10
283 atc ctg gac caa agg aat cgg cag gtg acg ttc acc aag cgg aag ttc 520
284 Ile Leu Asp Gln Arg Asn Arg Gln Val Thr Phe Thr Lys Arg Lys Phe
285           15                      20                      25
287 ggg ctg atg aag aag gcc tat gag ctg agc gtg ctc tgt gac tgt gag 568
288 Gly Leu Met Lys Lys Ala Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu
289           30                      35                      40
291 ata gcc ctc atc atc ttc aac agc gcc aac cgc ctc ttc cag tat gcc 616
292 Ile Ala Leu Ile Ile Phe Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala
293       45                      50                      55
295 agc acg gac atg gac cgt gtg ctg ctg aag tac aca gag tac agc gag 664
296 Ser Thr Asp Met Asp Arg Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu

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Use of n and / or X has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa

VERIFICATION SUMMARY

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Input Set : A:\LJ4714.txt

Output Set: N:\CRF3\03252002\I876187.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:976 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:978 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1029 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1082 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1084 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21